SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-2.p2n.rnpbm.

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-2.p2n.rnpbm.

start

```
                        GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on:         August  7, 2006, 14:46:45 ; Search time 1495 Seconds
                                            (without alignments)
                                            5868.476 Million cell updates/sec

Title:          US -10-679-362-2
Perfect score:  2469
Sequence:       1 MSTQRLRNEDYHDYSSTDVS..........YELIQPSNAPIFINSTCAFI 476

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:     37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model  -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10679362/runat_07082006_113052_26046/app_query.fasta_1
-DB=Published_Applications_NA_Main  -QFMT=fastap  -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10679362_@CGN_1_1_2530_@runat_07082006_113052_26046  -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      Published_Applications_NA_Main:*
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                2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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                11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
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13:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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16:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2469	100.0	1597	7	US -10-120-988-9	Sequence 9, Appli
2	2469	100.0	2055	7	US -10-225-810-5	Sequence 5, Appli
3	2469	100.0	2093	3	US-09-805-456-1	Sequence 1, Appli
4	2469	100.0	2093	8	US -10-679-362-1	Sequence 1, Appli
5	2469	100.0	5821	10	US -10-887-553A-1194	Sequence 1194, Ap
6	2460	99.6	1501	7	US -10-080-334-21	Sequence 21, Appl
7	2402.5	97.3	3114	8	US -10-332-447-40	Sequence 40, Appl
8	2398	97.1	1513	7	US -10-080-334-19	Sequence 19, Appl
9	2217	89.8	1961	7	US -10-094-749-1437	Sequence 1437, Ap
10	2146.5	86.9	1824	7	US -10-225-810-42	Sequence 42, Appl
11	2137.5	86.6	2034	7	US -10-225-810-2	Sequence 2, Appli
12	1722.5	69.8	3434	7	US -10-225-810-3	Sequence 3, Appli
13	1718.5	69.6	1464	7	US -10-392-219-1	Sequence 1, Appli
14	1718.5	69.6	2142	8	US -10-467-685-27	Sequence 27, Appl
15	1697.5	68.8	2456	7	US -10-225-810-13	Sequence 13, Appl
16	1676.5	67.9	2436	7	US -10-225-810-6	Sequence 6, Appli
17	1676.5	67.9	2436	7	US -10-225-810-55	Sequence 55, Appl
18	1476.5	59.8	1703	7	US -10-225-810-4	Sequence 4, Appli
19	1452.5	58.8	1473	6	US -10-291-737-1	Sequence 1, Appli
20	1452.5	58.8	1473	7	US -10-365-564-1	Sequence 1, Appli
21	1420	57.5	1752	7	US -10-225-810-1	Sequence 1, Appli
22	1333.5	54.0	947	9	US -10-357-930-23233	Sequence 23233, A
23	1333.5	54.0	947	9	US -10-357-930-29106	Sequence 29106, A
24	1263	51.2	953	7	US -10-080-334-23	Sequence 23, Appl
25	1255.5	50.9	1455	6	US -10-055-025-3	Sequence 3, Appli
26	1255.5	50.9	1455	7	US -10-154-419-93	Sequence 93, Appl
27	1255.5	50.9	1455	16	US -11-043-889-53	Sequence 53, Appl
28	1255.5	50.9	2397	6	US -10-055-025-1	Sequence 1, Appli
29	1255.5	50.9	2397	7	US -10-154-419-91	Sequence 91, Appl
30	1255.5	50.9	2397	16	US -11-043-889-51	Sequence 51, Appl
31	1255.5	50.9	2423	6	US -10-098-841-260	Sequence 260, App
32	1255.5	50.9	2905	8	US -10-755-889-21	Sequence 21, Appl
33	1255.5	50.9	3038	7	US -10-168-651-50	Sequence 50, Appl
34	1201.5	48.7	1916	7	US -10-108-260A-1166	Sequence 1166, Ap
35	1201.5	48.7	3076	9	US -10-723-860-5256	Sequence 5256, Ap
36	1173	47.5	739	10	US -10-450-763-26457	Sequence 26457, A
37	1156	46.8	1913	7	US -10-225-810-40	Sequence 40, Appl
38	1088	44.1	986	7	US -10-225-810-50	Sequence 50, Appl
39	989.5	40.1	1615	8	US -10-415-378-30	Sequence 30, Appl
40	866	35.1	2036	13	US -11-097-143-26834	Sequence 26834, A
41	861	34.9	1863	13	US -11-097-143-31109	Sequence 31109, A
42	861	34.9	2140	13	US -11-097-143-26192	Sequence 26192, A
43	826	33.5	13894	7	US -10-225-810-8	Sequence 8, Appli
44	790	32.0	4291	13	US -11-097-143-31108	Sequence 31108, A
45	790	32.0	5956	13	US -11-097-143-26191	Sequence 26191, A

ALIGNMENTS

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RESULT 1
US-10-120-988-9
; Sequence 9, Application US/10120988
; Publication No. US20030219745A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Goodrich, Ryle
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. US20030219745A1el Nucleic Acids and
```

SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-2.p2n.rnpbn.

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-2.p2n.rnpbn.

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                      GenCore version 5.1.9
          Copyright (c) 1993  - 2006  Bioacceleration Ltd.


OM protein - nucleic search, using frame_plus_p2n model

Run on:        August  7, 2006, 14:51:51 ; Search time 235 Seconds
                                    (without alignments)
                                    4812.163 Million cell updates/sec

Title:         US -10-679-362-2
Perfect score: 2469
Sequence:      1 MSTQRLRNEDYHDYSSTDVS.........YELIQPSNAPIFINSTCAFI 476

Scoring table: BLOSUM62
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               Ygapop 10.0 , Ygapext  0.5
               Fgapop  6.0 , Fgapext  7.0
               Delop   6.0 , Delext   7.0

Searched:      2193277 seqs, 791917567 residues

Total number of hits satisfying chosen parameters:      4386554

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model  -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10679362/runat_07082006_113054_26104/app_query.fasta_1
-DB=Published_Applications_NA_New  -QFMT=fastap  -SUFFIX=p2n.rnpbn  -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss03h
-USER=US10679362_@CGN_1_1_207_@runat_07082006_113054_26104   -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :     Published_Applications_NA_New:*
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               2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
               3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
               4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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               8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
               9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2469	100.0	5821	8	US -11-266-748A-31080	Sequence 31080, A
2	2469	100.0	5821	8	US -11-266-748A-56815	Sequence 56815, A
3	2469	100.0	5823	8	US -11-266-748A-28306	Sequence 28306, A
4	1255.5	50.9	2426	6	US -10-505-928-27	Sequence 27, Appl
5	1255.5	50.9	2493	8	US -11-266-748A-31287	Sequence 31287, A
6	1244.5	50.4	1869	8	US -11-266-748A-27590	Sequence 27590, A
7	1201.5	48.7	1916	8	US -11-293-697-1166	Sequence 1166, Ap
8	552.5	22.4	1625	8	US -11-266-748A-94144	Sequence 94144, A
9	552.5	22.4	1625	8	US-11-266-748A-113171	Sequence 113171,
c 10	552.5	22.4	1625	8	US -11-266-748A-146955	Sequence 146955,
c 11	503	20.4	586	8	US -11-266-748A-94145	Sequence 94145, A
c 12	503	20.4	586	8	US -11-266-748A-113172	Sequence 113172,
13	503	20.4	586	8	US -11-266-748A-146956	Sequence 146956,
14	468	19.0	1588	6	US -10-953-349-367	Sequence 367, App
15	465.5	18.9	2142	8	US -11-217-529-78323	Sequence 78323, A
16	453.5	18.4	2154	8	US -11-217-529-2181	Sequence 2181, Ap
17	418	16.9	2160	8	US -11-217-529-4562	Sequence 4562, Ap
18	410.5	16.6	494	8	US -11-266-748A-351476	Sequence 351476
c 19	410.5	16.6	494	8	US -11-266-748A-434855	Sequence 434855,
20	405	16.4	1500	6	US -10-449-902-8554	Sequence 8554, Ap
21	405	16.4	1514	6	US -10-449-902-20813	Sequence 20813, A
22	404.5	16.4	1756	6	US -10-449-902-4377	Sequence 4377, Ap
23	404.5	16.4	2089	6	US -10-449-902-25208	Sequence 25208, A
24	402.5	16.3	2977	6	US -10-449-902-25143.	Sequence 25143, A
25	400	16.2	1405	6	US -10-449-902-786	Sequence 786, App
26	392.5	15.9	2200	9	US -11-218-305-9533	Sequence 9533, Ap
27	387.5	15.7	2079	8	US -11-217-529-77476	Sequence 77476, A
28	386.5	15.7	1697	6	US -10-449-902-4221	Sequence 4221, Ap
29	379.5	15.4	1984	6	US -10-449-902-14209	Sequence 14209, A
30	352.5	14.3	1381	6	US -10-449-902-8460	Sequence 8460, Ap
31	323.5	13.1	1354	8	US -11-145-307A-6	Sequence 6, Appli
32	320	13.0	2000	9	US -11-174-307B-5169	Sequence 5169, Ap
33	307.5	12.5	1623	9	US -11-056-355B-54598	Sequence 54598, A
34	302	12.2	2007	9	US -11-056-355B-105674	Sequence 105674,
35	302	12.2	2007	9	US -11-056-355B-116913	Sequence 116913,
36	296	12.0	2160	9	US -11-218-305-13745	Sequence 13745, A
37	292	11.8	1534	9	US -11-218-305-13746	Sequence 13746, A
38	292	11.8	1829	9	US -11-056-355B-79661	Sequence 79661, A
39	291.5	11.8	1614	9	US -11-056-355B-75676	Sequence 75676, A
40	290	11.7	2112	9	US -11-218-305-10108	Sequence 10108, A
41	281	11.4	2011	9	US -11-056-355B-96648	Sequence 96648, A
42	276	11.2	2010	9	US -11-056-355B-36516	Sequence 36516, A
43	276	11.2	2010	9	US -11-056-355B-44878	Sequence 44878, A
44	268.5	10.9	1859	6	US -10-953-349-34885	Sequence 34885, A
45	268.5	10.9	1859	9	US -11-056-355B-8579	Sequence 8579, Ap

ALIGNMENTS

RESULT 1
US-11-266-748A-31080
; Sequence 31080, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815 -0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005 -11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004 -11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004 -11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4

SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-1.rnpbm.

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-1.rnpbm.

start

```
                         GenCore version 5.1.9
              Copyright (c) 1993  - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:        August  7, 2006, 14:01:19 ; Search time 2620 Seconds
                                           (without alignments)
                                           9816.038 Million cell updates/sec

Title:         US -10-679-362-1
Perfect score: 2093
Sequence:      1 cgggcagcaaaggaggatgg..........aaaaaaaaaaaaaaaaaaaa 2093

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:      37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published_Applications_NA_Main:*
                1:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                3:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                5:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                6:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                7:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                8:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                9:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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                11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                     %
Result           Query
   No.   Score  Match Length DB  ID                  Description
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    1    2093  100.0   2093  3   US -09-805-456-1         Sequence 1, Appli
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    2    2093   100.0   2093    8   US -10-679-362-1           Sequence 1, Appli
    3   1847.6   88.3   2055    7   US -10-225-810-5           Sequence 5, Appli
    4   1806.4   86.3   5821   10   US -10-887-553A-1194         Sequence 1194, Ap
    5   1609.8   76.9   3114    8   US -10-332-447-40          Sequence 40, Appl
    6   1541.8   73.7   1961    7   US -10-094-749-1437        Sequence 1437, Ap
    7   1498.4   71.6   1597    7   US -10-120-988-9           Sequence 9, Appli
    8   1441.8   68.9   1501    7   US -10-080-334-21          Sequence 21, Appl
    9   1363.8   65.2   1513    7   US -10-080-334-19          Sequence 19, Appl
   10   1125.8   53.8   1824    7   US -10-225-810-42          Sequence 42, Appl
   11   1113.8   53.2   2034    7   US -10-225-810-2           Sequence 2, Appli
   12    869.2   41.5   2142    8   US -10-467-685-27          Sequence 27, Appl
   13    867.6   41.5   3434    7   US -10-225-810-3           Sequence 3, Appli
   14     866    41.4   1464    7   US -10-392-219-1           Sequence 1, Appli
   15    830.2   39.7   2436    7   US -10-225-810-6           Sequence 6, Appli
   16    830.2   39.7   2436    7   US -10-225-810-55          Sequence 55, Appl
   17    829.8   39.6   2456    7   US -10-225-810-13          Sequence 13, Appl
   18    769.6   36.8    947    9   US -10-357-930-23233       Sequence 23233, A
   19    769.6   36.8    947    9   US -10-357-930-29106       Sequence 29106, A
   20    729.8   34.9   1703    7   US -10-225-810-4           Sequence 4, Appli
   21    727.4   34.8    953    7   US -10-080-334-23          Sequence 23, Appl
   22    721.8   34.5   1473    6   US -10-291-737-1           Sequence 1, Appli
   23    721.8   34.5   1473    7   US -10-365-564-1           Sequence 1, Appli
   24    682     32.6   1752    7   US -10-225-810-1           Sequence 1, Appli
   25    681.8   32.6    739   10   US -10-450-763-26457        Sequence 26457, A
c  26    645.2   30.8  77992    7   US -10-225-810-11          Sequence 11, Appl
c  27    645.2   30.8 250000    7   US -10-225-810-26          Sequence 26, Appl
   28    634.2   30.3  46649    3   US -09-805-456-3           Sequence 3, Appli
   29    634.2   30.3  46649    8   US -10-679-362-3           Sequence 3, Appli
   30    586.4   28.0   1913    7   US -10-225-810-40          Sequence 40, Appl
   31    569.8   27.2    986    7   US -10-225-810-50          Sequence 50, Appl
   32    454.8   21.7   1615    8   US -10-415-378-30          Sequence 30, Appl
   33    422     20.2   3351    9   US -10-357-930-20872       Sequence 20872, A
   34    422     20.2   3351    9   US -10-357-930-21002       Sequence 21002, A
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ALIGNMENTS

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; Publication No. US20030170778A1
; GENERAL INFORMATION:
;   APPLICANT: WEI, Ming -Hui
;   TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
;   TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: CL001062
;   CURRENT APPLICATION NUMBER: US/09/805,456
;   CURRENT FILING DATE: 2001 -03-14
;   NUMBER OF SEQ ID NOS: 7
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2093
;   TYPE: DNA
;   ORGANISM: Human
US-09-805-456-1

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SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-1.rnpbn.

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-1.rnpbn.

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                           GenCore version 5.1.9
                  Copyright (c) 1993  - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

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; Sequence 31080, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815 -0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005 -11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004 -11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004 -11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004 -11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004 -11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004 -11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004 -11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005 -03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005 -07-18
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; SOFTWARE: PatentIn version 3.3
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